



SEQUENCE LISTING

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Immusol Incorporated

<120> siRNA Libraries Optimized for Predetermined Protein Families

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<140> US 10/776,399

<141> 2004-02-10

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<170> PatentIn version 3.2

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 <213> Homo sapiens

 <400> 257
 cacaattatg tccaccggga cctggctgcc agaaacatct tggatgaat 48

 <210> 258
 <211> 16
 <212> PRT
 <213> Homo sapiens

 <400> 258

 His Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn
 1 5 10 15

 <210> 259
 <211> 48
 <212> DNA
 <213> Homo sapiens

 <400> 259
 aggggaagtca tccacaaaga cctggctgcc aggaactgtg tcattgat 48

 <210> 260
 <211> 16
 <212> PRT
 <213> Homo sapiens

 <400> 260

 Arg Glu Val Ile His Lys Asp Leu Ala Ala Arg Asn Cys Val Ile Asp
 1 5 10 15

 <210> 261
 <211> 48
 <212> DNA
 <213> Homo sapiens

 <400> 261
 aaccgctttg tgcataagga cttggctgcg cgtaactgcc tggtcagt 48

 <210> 262
 <211> 16
 <212> PRT
 <213> Homo sapiens

 <400> 262

 Asn Arg Phe Val His Lys Asp Leu Ala Ala Arg Asn Cys Leu Val Ser
 1 5 10 15

<210> 263
<211> 48
<212> DNA
<213> Homo sapiens

<400> 263
cacttctttg tccacaagga ccttgcagct cgcaatattt taatcgga

48

<210> 264
<211> 16
<212> PRT
<213> Homo sapiens

<400> 264

His	Phe	Phe	Val	His	Lys	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Ile	Gly
1				5				10					15		

<210> 265
<211> 48
<212> DNA
<213> Homo sapiens

<400> 265
aatcacttca tccacagggga tattgccgcc cggaactgcc tgctgagc

48

<210> 266
<211> 16
<212> PRT
<213> Homo sapiens

<400> 266

Asn	His	Phe	Ile	His	Arg	Asp	Ile	Ala	Ala	Arg	Asn	Cys	Leu	Leu	Ser
1				5				10					15		

<210> 267
<211> 48
<212> DNA
<213> Homo sapiens

<400> 267
aaccacttca tccaccgaga cattgctgcc agaaactgcc tcttgacc

48

<210> 268
<211> 16
<212> PRT
<213> Homo sapiens

<400> 268

Asn	His	Phe	Ile	His	Arg	Asp	Ile	Ala	Ala	Arg	Asn	Cys	Leu	Leu	Thr
1				5				10					15		

<210> 269
 <211> 54
 <212> DNA
 <213> Artificial

 <220>
 <223> variant 1 semi-randomized oligonucleotide for tyrosine
 kinase family portion of catalytic domain

 <220>
 <221> modified_base
 <222> (1)..(1)
 <223> n = c modified by 5' phosphate

 <400> 269
 ncaggacgac aaaaagacht gygarggstg yaargghctt tttaggcttt tcgg 54

 <210> 270
 <211> 54
 <212> DNA
 <213> Artificial

 <220>
 <223> variant 2 semi-randomized oligonucleotide for tyrosine
 kinase family portion of catalytic domain

 <220>
 <221> modified_base
 <222> (1)..(1)
 <223> n = c modified by 5' phosphate

 <220>
 <221> modified_base
 <222> (37)..(37)
 <223> n = g, a, c, or t

 <400> 270
 ncaggacgac aaaaagwsyt gygarggbtg caarggnctt tttaggcttt tcgg 54

 <210> 271
 <211> 54
 <212> DNA
 <213> Artificial

 <220>
 <223> variant 3 semi-randomized oligonucleotide for tyrosine
 kinase family portion of catalytic domain

 <220>
 <221> modified_base
 <222> (1)..(1)
 <223> n = c modified by 5' phosphate

 <400> 271
 ncaggacgac aaaaagacst gcgagggtg caaragycctt tttaggcttt tcgg 54

<210> 272
 <211> 53
 <212> DNA
 <213> Artificial

 <220>
 <223> variant 4 semi-randomized oligonucleotide for tyrosine
 kinase family portion of catalytic domain

 <220>
 <221> modified_base
 <222> (1)..(1)
 <223> n = c modified by 5' phosphate

 <400> 272
 ncaggacgac aaaaagcctg cracggctgc wsmggycctt ttaggctttt cgg 53

<210> 273
 <211> 54
 <212> DNA
 <213> Artificial

 <220>
 <223> variant 5 semi-randomized oligonucleotide for tyrosine
 kinase family portion of catalytic domain

 <220>
 <221> modified_base
 <222> (1)..(1)
 <223> n = c modified by 5' phosphate

 <400> 273
 ncaggacgac aaaaagasct gtgayggstg caagggycct ttaggctttt tcgg 54

<210> 274
 <211> 53
 <212> DNA
 <213> Artificial

 <220>
 <223> variant 6 semi-randomized oligonucleotide for tyrosine
 kinase family portion of catalytic domain

 <220>
 <221> modified_base
 <222> (1)..(1)
 <223> n = c modified by 5' phosphate

 <220>
 <221> modified_base
 <222> (18)..(18)
 <223> n = g, a, c, or t

 <400> 274
 ncaggacgac aaaaagcntg ygarggvtgy aagggycctt ttaggctttt cgg 53

<210> 275
 <211> 54
 <212> DNA
 <213> Artificial

 <220>
 <223> variant 7 semi-randomized oligonucleotide for tyrosine
 kinase family portion of catalytic domain

 <220>
 <221> modified_base
 <222> (1)..(1)
 <223> n = c modified by 5' phosphate

 <220>
 <221> modified_base
 <222> (19)..(19)
 <223> n = g, a, c, or t

 <400> 275
 ncaggacgac aaaaagacnt gtgarrgmtg caaggghctt tttaggcttt tcgg 54

 <210> 276
 <211> 54
 <212> DNA
 <213> Artificial

 <220>
 <223> variant 8 semi-randomized oligonucleotide for tyrosine
 kinase family portion of catalytic domain

 <220>
 <221> modified_base
 <222> (1)..(1)
 <223> n = c modified by 5' phosphate

 <400> 276
 ncaggacgac aaaaagacht gtggvagctg yaargtyctt tttaggcttt tcgg 54

 <210> 277
 <211> 53
 <212> DNA
 <213> Artificial

 <220>
 <223> variant 7 semi-randomized oligonucleotide for tyrosine
 kinase family portion of catalytic domain

 <220>
 <221> modified_base
 <222> (1)..(1)
 <223> n = c modified by 5' phosphate

 <400> 277
 ncaggacgac aaaaagtcst gygargshtg yaargccttt ttaggctttt cgg 53

<210> 278
 <211> 20
 <212> DNA
 <213> Artificial

 <220>
 <223> adapter oligonucleotide Univ-1(FseI)

 <400> 278
 ctttttgtcg tcctggccgg 20

<210> 279
 <211> 21
 <212> DNA
 <213> Artificial

 <220>
 <223> adapter oligonucleotide Univ-2(AscI)

 <220>
 <221> modified_base
 <222> (1)..(1)
 <223> n = c modified by 5' phosphate

 <400> 279
 ngcgccgaaa agcctaataaa g 21

<210> 280
 <211> 569
 <212> DNA
 <213> Artificial

 <220>
 <223> human U6/murine U6 opposing promoter cassette

 <400> 280
 ggatccaagc ttaaggctcg gcaggaagag ggcctatttc ccatgattcc ttcattttg 60
 catatacgat acaaggctgt tagagagata attagaatta atttgactgt aaacacaaag 120
 atattagtac aaaatacgtg acgtagaaaag taataatttc ttgggtagtt tgcagtttta 180
 aaattatggt ttaaaatgga ctatcatatg cttaccgtaa cttgaaagta tttcgatttc 240
 ttggctttat atatcggccg gcctcgaggc gcgccatatt tatagtctca aaacacacaa 300
 ttactttaca gttaggggtga gtttcctttt gtgctgtttt ttaaaataat aatttagtat 360
 ttgtatctct tatagaaatc caagcctatc atgtaaaatg tagctagtat taaaaagaac 420
 agattatctg tcttttatcg cacattaagc ctctatagtt actaggaaat attatatgca 480
 aattaaccgg ggcaggggag tagccgagct tctcccacaa gtctgtgcga gggggccggc 540
 gcgggcctag agatggcggc gtcggatcc 569

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<210> 281
<211> 21
<212> DNA
<213> Artificial

<220>
<223> nuclear hormone receptor family zinc finger domain
      (ZnF_C4 domain) consensus sequence (21 nt)

<220>
<221> modified_base
<222> (1)..(21)
<223> n = g, a, c or t

<400> 281
dyntgyrrnr sntgywvvr b n
21

<210> 282
<211> 7
<212> PRT
<213> Artificial

<220>
<223> tyrosine kinase family portion of catalytic domain
      variant 1 signature motif

<400> 282
His Arg Asp Leu Lys Ser Ser
  1             5

<210> 283
<211> 7
<212> PRT
<213> Artificial

<220>
<223> tyrosine kinase family portion of catalytic domain
      variant 2 signature motif

<220>
<221> MOD_RES
<222> (4)
<223> Xaa = Leu, Val or Ile

<220>
<221> MOD_RES
<222> (6)
<223> Xaa = Ala or Val

<400> 283
His Arg Asx Xaa Ala Xaa Arg
  1             5

<210> 284
<211> 7
<212> PRT
<213> Artificial

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<220>
<223> tyrosine kinase family portion of catalytic domain
variant 3 signature motif

<220>
<221> MOD_RES
<222> (6)
<223> Xaa = Ala or Ser

<400> 284

His Arg Asp Leu Arg Xaa Ala
1 5

<210> 285
<211> 7
<212> PRT
<213> Artificial

<220>
<223> tyrosine kinase family portion of catalytic domain
variant 4 signature motif

<220>
<221> MOD_RES
<222> (2)
<223> Xaa = Arg or Lys

<400> 285

His Xaa Asp Leu Ala Thr Arg
1 5

<210> 286
<211> 7
<212> PRT
<213> Artificial

<220>
<223> tyrosine kinase family portion of catalytic domain
variant 5 signature motif

<400> 286

His Arg Asp Leu Ala Ala Arg
1 5

<210> 287
<211> 7
<212> PRT
<213> Artificial

<220>
<223> tyrosine kinase family portion of catalytic domain
variant 6 signature motif

<400> 287

His Lys Asp Leu Ala Ala Arg
1 5

<210> 288

<211> 7

<212> PRT

<213> Artificial

<220>

<223> tyrosine kinase family portion of catalytic domain
variant 7 signature motif

<400> 288

His Arg Asp Ile Ala Ala Arg
1 5

<210> 289

<211> 19

<212> DNA

<213> Artificial

<220>

<223> nuclear hormone receptor family zinc finger domain
(ZnF_C4 domain) consensus sequence (19 nt)

<220>

<221> modified_base

<222> (1)..(19)

<223> n = g, a, c or t

<400> 289

dyntgyrrnr sntgywvvr

19

<210> 290

<211> 21

<212> DNA

<213> Artificial

<220>

<223> tyrosine kinase family portion of catalytic domain
variant 1 consensus sequence

<400> 290

caccgsgacc tyaagtccag c

21

<210> 291

<211> 21

<212> DNA

<213> Artificial

<220>

<223> tyrosine kinase family portion of catalytic domain
variant 2 consensus sequence

<400> 291
 caymgrracv tkgcwgyscg d 21

<210> 292
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> tyrosine kinase family portion of catalytic domain
 variant 3 consensus sequence

<220>
 <221> modified_base
 <222> (9)
 <223> n = g, a, c or t

<400> 292
 caymgngayc tbmgdkcdgc h 21

<210> 293
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> tyrosine kinase family portion of catalytic domain
 variant 4 consensus sequence

<400> 293
 cacmrvgayy tvgchacvmg v 21

<210> 294
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> tyrosine kinase family portion of catalytic domain
 variant 5 consensus sequence

<220>
 <221> modified_base
 <222> (1)..(21)
 <223> n = g, a, c or t

<400> 294
 caymgngayy tngcngcnmg n 21

<210> 295
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> tyrosine kinase family portion of catalytic domain
 variant 6 consensus sequence

<400> 295
 cayaargacy tkgcwgcbbmg b 21

<210> 296
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> tyrosine kinase family portion of catalytic domain
 variant 7 consensus sequence

<400> 296
 cacmrgaya ttgcygccmg r 21

<210> 297
 <211> 7
 <212> PRT
 <213> Artificial

<220>
 <223> nuclear hormone receptor family zinc finger domain
 (ZnF_C4 domain) variant 1 signature motif

<400> 297
 Thr Cys Glu Gly Cys Lys Gly
 1 5

<210> 298
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> nuclear hormone receptor family zinc finger domain
 (ZnF_C4 domain) variant 1 consensus sequence

<400> 298
 achtgygarg gstgyaargg h 21

<210> 299
 <211> 7
 <212> PRT
 <213> Artificial

<220>
 <223> nuclear hormone receptor family zinc finger domain
 (ZnF_C4 domain) variant 2 signature motif

<400> 299
 Ser Cys Glu Gly Cys Lys Gly
 1 5

<210> 300
 <211> 21
 <212> DNA
 <213> Artificial

 <220>
 <223> nuclear hormone receptor family zinc finger domain
 (ZnF_C4 domain) variant 2 consensus sequence

 <220>
 <221> modified_base
 <222> (21)
 <223> n = g, a, c or t

 <400> 300
 wsytgygarg gbtgcaargg n 21

 <210> 301
 <211> 7
 <212> PRT
 <213> Artificial

 <220>
 <223> nuclear hormone receptor family zinc finger domain
 (ZnF_C4 domain) variant 3 signature motif

 <400> 301
 Thr Cys Glu Gly Cys Lys Ser
 1 5

 <210> 302
 <211> 21
 <212> DNA
 <213> Artificial

 <220>
 <223> nuclear hormone receptor family zinc finger domain
 (ZnF_C4 domain) variant 3 consensus sequence

 <400> 302
 acstgcgagg gctgcaarag y 21

 <210> 303
 <211> 7
 <212> PRT
 <213> Artificial

 <220>
 <223> nuclear hormone receptor family zinc finger domain
 (ZnF_C4 domain) variant 4 signature motif

 <400> 303
 Ala Cys Asx Gly Cys Ser Gly
 1 5

<210> 304
 <211> 21
 <212> DNA
 <213> Artificial

 <220>
 <223> nuclear hormone receptor family zinc finger domain
 (ZnF_C4 domain) variant 4 consensus sequence

 <400> 304
 gcctgcracg gctgcwsmgg y 21

 <210> 305
 <211> 7
 <212> PRT
 <213> Artificial

 <220>
 <223> nuclear hormone receptor family zinc finger domain
 (ZnF_C4 domain) variant 5 signature motif

 <220>
 <221> MOD_RES
 <222> (1)
 <223> Xaa = Thr or Ser

 <400> 305

 Xaa Cys Asp Gly Cys Lys Gly
 1 5

 <210> 306
 <211> 21
 <212> DNA
 <213> Artificial

 <220>
 <223> nuclear hormone receptor family zinc finger domain
 (ZnF_C4 domain) variant 5 consensus sequence

 <400> 26
 asctgtgayg gstgcaaggg y 21

 <210> 307
 <211> 7
 <212> PRT
 <213> Artificial

 <220>
 <223> nuclear hormone receptor family zinc finger domain
 (ZnF_C4 domain) variant 6 signature motif

 <400> 27

 Ala Cys Glu Gly Cys Lys Gly
 1 5

<210> 308
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> nuclear hormone receptor family zinc finger domain
 (ZnF_C4 domain) variant 6 consensus sequence

<220>
 <221> modified_base
 <222> (3)
 <223> n = g, a, c or t

<400> 308
 gcntgygarg gvtgyaagg y

21

<210> 309
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> nuclear hormone receptor family zinc finger domain
 (ZnF_C4 domain) variant 7 signature motif

<220>
 <221> MOD_RES
 <222> (4)
 <223> Xaa = Gly or Ser

<400> 309

Thr Cys Glu Xaa Cys Lys Gly
 1 5

<210> 310
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> nuclear hormone receptor family zinc finger domain
 (ZnF_C4 domain) variant 7 consensus sequence

<220>
 <221> modified_base
 <222> (3)
 <223> n = g, a, c or t

<400> 310
 acntgtgarr gmtgcaagg h

21

<210> 311
 <211> 7
 <212> PRT
 <213> Artificial

<220>
 <223> nuclear hormone receptor family zinc finger domain
 (ZnF_C4 domain) variant 8 signature motif
 <400> 311

Thr Cys Gly Ser Cys Lys Val
 1 5

<210> 312
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> nuclear hormone receptor family zinc finger domain
 (ZnF_C4 domain) variant 8 consensus sequence

<400> 312
 achtgtggva gctgyaargt h

21

<210> 313
 <211> 7
 <212> PRT
 <213> Artificial

<220>
 <223> nuclear hormone receptor family zinc finger domain
 (ZnF_C4 domain) variant 9 signature motif

<220>
 <221> MOD_RES
 <222> (4)
 <223> Xaa = Ala or Gly

<400> 313

Ser Cys Glu Xaa Cys Lys Ala
 1 5

<210> 314
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> nuclear hormone receptor family zinc finger domain
 (ZnF_C4 domain) variant 9 consensus sequence

<400> 314
 tcstgygarg shtgyaargc c

21